

# SEQUENCE LISTING

<110> Hayward, Nicholas K.  
 Weber, Gunther  
 Grimmond, Sean  
 Nordenskjold, Magnus  
 Larsson, Catharina

<120> A NOVEL GROWTH FACTOR AND A GENETIC SEQUENCE ENCODING  
 SAME

<130> Dav. Col. Cave

<140> 09/349,954  
 <141> 1999-07-08

<150> 08/765,588  
 <151> 1996-02-22

<160> 22

<170> PatentIn Ver. 2.1

<210> 1  
 <211> 649  
 <212> DNA  
 <213> Nucleotide Sequence of VEGF165

<220>  
 <221> CDS  
 <222> (17)..(589)

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 1 5 10  
 gcc ttg ctg ctc tac ctc cac cat gcc aag tgg tcc cag gct gca ccc 100  
 Ala Leu Leu Leu Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro  
 15 20 25  
 atg gca gaa gga gga ggg cag aat cat cac gaa gtg gtg aag ttc atg 148  
 Met Ala Glu Gly Gly Gly Gln Asn His His Glu Val Val Lys Phe Met  
 30 35 40  
 gat gtc tat cag cgc agc tac tgc cat cca atc gag acc ctg gtg gac 196  
 Asp Val Tyr Gln Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp  
 45 50 55 60  
 atc ttc cag gag tac cct gat gag atc gag tac atc ttc aag cca tcc 244

Ile Phe Gln Glu Tyr	Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser	
65	70	75
tgt gtg ccc ctg atg cga tgc ggg ggc tgc tgc aat gac gag ggc ctg		292
Cys Val Pro Leu Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu		
80	85	90
gag tgt gtg ccc act gag gag tcc aac atc acc atg cag att atg cgg		340
Glu Cys Val Pro Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg		
95	100	105
atc aaa cct cac caa ggc cag cac ata gga gag atg agc ttc cta cag		388
Ile Lys Pro His Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln		
110	115	120
cac aac aaa tgt gaa tgc aga cca aag aaa gat aga gca aga caa gaa		436
His Asn Lys Cys Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu		
125	130	135
aat ccc tgt ggg cct tgc tca gag cgg aga aag cat ttg ttt gta caa		484
Asn Pro Cys Gly Pro Cys Ser Glu Arg Arg Lys His Leu Phe Val Gln		
145	150	155
gat ccg cag acg tgt aaa tgt tcc tgc aaa aac aca gac tcg cgt tgc		532
Asp Pro Gln Thr Cys Lys Cys Ser Cys Lys Asn Thr Asp Ser Arg Cys		
160	165	170
aag gcg agg cag ctt gag tta aac gaa cgt act tgc aga tgt gac aag		580
Lys Ala Arg Gln Leu Glu Leu Asn Glu Arg Thr Cys Arg Cys Asp Lys		
175	180	185
ccg agg cgg tgagccgggc aggaggaagg agcctccctc agcgtttcgg		629
Pro Arg Arg		
190		
gaaccagatc tctcaccagg		649

<210> 2  
 <211> 191  
 <212> PRT  
 <213> Nucleotide Sequence of VEGF165

<400> 2															
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Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro Met Ala Glu Gly  
                     20                    25                    30  
 Gly Gly Gln Asn His His Glu Val Val Lys Phe Met Asp Val Tyr Gln  
                     35                    40                    45  
 Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu  
                     50                    55                    60  
 Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu  
                     65                    70                    75                    80  
 Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu Glu Cys Val Pro  
                     85                    90                    95  
 Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg Ile Lys Pro His  
                     100                    105                    110  
 Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln His Asn Lys Cys  
                     115                    120                    125  
 Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu Asn Pro Cys Gly  
                     130                    135                    140  
 Pro Cys Ser Glu Arg Arg Lys His Leu Phe Val Gln Asp Pro Gln Thr  
                     145                    150                    155                    160  
 Cys Lys Cys Ser Cys Lys Asn Thr Asp Ser Arg Cys Lys Ala Arg Gln  
                     165                    170                    175  
 Leu Glu Leu Asn Glu Arg Thr Cys Arg Cys Asp Lys Pro Arg Arg  
                     180                    185                    190

<210> 3  
 <211> 1094  
 <212> DNA  
 <213> Nucleotide Sequence of SOM175

<220>  
 <221> CDS  
 <222> (3)...(623)

<400> 3  
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     Met Ser Pro Leu Leu Arg Arg Leu Leu Leu Ala Ala Leu Leu Gln  
       1                    5                    10                    15  
 ctg gcc ccc gcc cag gcc cct gtc tcc cag cct gat gcc cct ggc cac 95  
 Leu Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His  
                     20                    25                    30

cag agg aaa gtg gtg tca tgg ata gat gtg tat act cgc gct acc tgc	143
Gln Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys	
35 40 45	
cag ccc cgg gag gtg gtg gtg ccc ttg act gtg gag ctc atg ggc acc	191
Gln Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr	
50 55 60	
gtg gcc aaa cag ctg gtg ccc agc tgc gtg act gtg cag cgc tgt ggt	239
Val Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly	
65 70 75	
ggc tgc tgc cct gac gat ggc ctg gag tgt gtg ccc act ggg cag cac	287
Gly Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His	
80 85 90 95	
caa gtc cgg atg cag atc ctc atg atc cgg tac ccg agc agt cag ctg	335
Gln Val Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu	
100 105 110	
ggg gag atg tcc ctg gaa gaa cac agc cag tgt gaa tgc aga cct aaa	383
Gly Glu Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys Arg Pro Lys	
115 120 125	
aaa aag gac agt gct gtg aag cca gac agg gct gcc act ccc cac cac	431
Lys Lys Asp Ser Ala Val Lys Pro Asp Arg Ala Ala Thr Pro His His	
130 135 140	
cgt ccc cag ccc cgt tct gtt ccg ggc tgg gac tct gcc ccc gga gca	479
Arg Pro Gln Pro Arg Ser Val Pro Gly Trp Asp Ser Ala Pro Gly Ala	
145 150 155	
ccc tcc cca gct gac atc acc cat ccc act cca gcc cca ggc ccc tct	527
Pro Ser Pro Ala Asp Ile Thr His Pro Thr Pro Ala Pro Gly Pro Ser	
160 165 170 175	
gcc cac gct gca ccc agc acc acc agc gcc ctg acc ccc gga cct gcc	575
Ala His Ala Ala Pro Ser Thr Thr Ser Ala Leu Thr Pro Gly Pro Ala	
180 185 190	
gct gcc gct gcc gac gcc gca gct tcc tcc gtt gcc aag ggc ggg gct	623
Ala Ala Ala Ala Asp Ala Ala Ala Ser Ser Val Ala Lys Gly Gly Ala	
195 200 205	

tagagctcaa cccagacacc tgcaggtgcc ggaagctgcy aaggtgacac atggcttttc 683  
 agactcagca ggggtgacttg cctcagagggc tatatcccag tgggggaaca aaggggagcc 743  
 tggtaaaaaa cagccaagcc cccaagacct cagcccaggc agaagctgct ctaggacctg 803  
 ggctctcag agggctcttc tgccatccct tgtctccctg aggccatcat caaacaggac 863  
 agagttggaa gaggagactg ggaggcagca agaggggtca cataccagct caggggagaa 923  
 tggagtactg tctcagtttc taaccactct gtgcaagtaa gcattctaca actggctctt 983  
 cctcccctca ctaagaagac ccaaactctt gcataatggg atttgggctt tgggtacaaga 1043  
 actgtgaccc ccaaccctga taaaagagat ggaaggaaaa aaaaaaaaaa a 1094

<210> 4  
 <211> 207  
 <212> PRT  
 <213> Nucleotide Sequence of SOM175

<400> 4  
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 Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His Gln  
 20 25 30  
 Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys Gln  
 35 40 45  
 Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr Val  
 50 55 60  
 Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly Gly  
 65 70 75 80  
 Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His Gln  
 85 90 95  
 Val Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu Gly  
 100 105 110  
 Glu Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys Arg Pro Lys Lys  
 115 120 125  
 Lys Asp Ser Ala Val Lys Pro Asp Arg Ala Ala Thr Pro His His Arg

130		135		140
Pro Gln Pro Arg Ser Val Pro Gly Trp Asp Ser Ala Pro Gly Ala Pro				
145		150	155	160
Ser Pro Ala Asp Ile Thr His Pro Thr Pro Ala Pro Gly Pro Ser Ala				
	165		170	175
His Ala Ala Pro Ser Thr Thr Ser Ala Leu Thr Pro Gly Pro Ala Ala				
	180		185	190
Ala Ala Ala Asp Ala Ala Ala Ser Ser Val Ala Lys Gly Gly Ala				
	195	200		205

<210> 5  
 <211> 993  
 <212> DNA  
 <213> Nuc. Seq. of SOM175 Absent Exon 6

<220>  
 <221> CDS  
 <222> (3)..(566)

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 Met Ser Pro Leu Leu Arg Arg Leu Leu Leu Ala Ala Leu Leu Gln  
 1 5 10 15  
 ctg gcc ccc gcc cag gcc cct gtc tcc cag cct gat gcc cct ggc cac 95  
 Leu Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His  
 20 25 30  
 cag agg aaa gtg gtg tca tgg ata gat gtg tat act cgc gct acc tgc 143  
 Gln Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys  
 35 40 45  
 cag ccc cgg gag gtg gtg gtg ccc ttg act gtg gag ctc atg ggc acc 191  
 Gln Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr  
 50 55 60  
 gtg gcc aaa cag ctg gtg ccc agc tgc gtg act gtg cag cgc tgt ggt 239  
 Val Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly  
 65 70 75  
 ggc tgc tgc cct gac gat ggc ctg gag tgt gtg ccc act ggg cag cac 287  
 Gly Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His  
 80 85 90 95

caa gtc cgg atg cag atc ctc atg atc cgg tac ccg agc agt cag ctg 335  
 Gln Val Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu  
 100 105 110  
 ggg gag atg tcc ctg gaa gaa cac agc cag tgt gaa tgc aga cct aaa 383  
 Gly Glu Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys Arg Pro Lys  
 115 120 125  
 aaa aag gac agt gct gtg aag cca gat agc ccc agg ccc ctc tgc cca 431  
 Lys Lys Asp Ser Ala Val Lys Pro Asp Ser Pro Arg Pro Leu Cys Pro  
 130 135 140  
 cgc tgc acc cag cac cac cag cgc cct gac ccc cgg acc tgc cgc tgc 479  
 Arg Cys Thr Gln His His Gln Arg Pro Asp Pro Arg Thr Cys Arg Cys  
 145 150 155  
 cgc tgc cga cgc cgc agc ttc ctc cgt tgc caa ggg cgg ggc tta gag 527  
 Arg Cys Arg Arg Arg Ser Phe Leu Arg Cys Gln Gly Arg Gly Leu Glu  
 160 165 170 175  
 ctc aac cca gac acc tgc agg tgc cgg aag ctg cga agg tgacacatgg 576  
 Leu Asn Pro Asp Thr Cys Arg Cys Arg Lys Leu Arg Arg  
 180 185  
 cttttcagac tcagcagggg gacttgccctc agaggctata tcccagtgagg ggaacaaagg 636  
 ggagcctggg aaaaaacagc caagccccca agacctcagc ccaggcagaa gctgctctag 696  
 gacctggggc tctcagaggg ctcttctgcc atcccttgct tccctgaggc catcatcaaa 756  
 caggacagag ttggaagagg agactgggag gcagcaagag gggtcacata ccagctcagg 816  
 ggagaatgga gtactgtctc agtttctaac cactctgtgc aagtaagcat cttacaactg 876  
 gctcttctc cctcactaa gaagacccaa acctctgcat aatgggattt gggctttggg 936  
 acaagaactg tgacccccaa ccctgataaa agagatggaa ggaaaaaaaa aaaaaaa 993

<210> 6  
 <211> 188  
 <212> PRT  
 <213> Nuc. Seq. of SOM175 Absent Exon 6

<400> 6  
Met Ser Pro Leu Leu Arg Arg Leu Leu Leu Ala Ala Leu Leu Gln Leu  
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Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His Gln  
20 25 30  
Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys Gln  
35 40 45  
Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr Val  
50 55 60  
Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly Gly  
65 70 75 80  
Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His Gln  
85 90 95  
Val Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu Gly  
100 105 110  
Glu Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys Arg Pro Lys Lys  
115 120 125  
Lys Asp Ser Ala Val Lys Pro Asp Ser Pro Arg Pro Leu Cys Pro Arg  
130 135 140  
Cys Thr Gln His His Gln Arg Pro Asp Pro Arg Thr Cys Arg Cys Arg  
145 150 155 160  
Cys Arg Arg Arg Ser Phe Leu Arg Cys Gln Gly Arg Gly Leu Glu Leu  
165 170 175  
Asn Pro Asp Thr Cys Arg Cys Arg Lys Leu Arg Arg  
180 185

<210> 7  
<211> 858  
<212> DNA  
<213> Nuc. Seq. of SOM175 Absent Exons 6&7

<220>  
<221> CDS  
<222> (3)..(431)

<400> 7  
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Met Ser Pro Leu Leu Arg Arg Leu Leu Leu Ala Ala Leu Leu Gln  
1 5 10 15  
ctg gcc ccc gcc cag gcc cct gtc tcc cag cct gat gcc cct ggc cac 95



Leu Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His  
                     20                    25                    30  
 cag agg aaa gtg gtg tca tgg ata gat gtg tat act cgc gct acc tgc 143  
 Gln Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys  
                     35                    40                    45  
 cag ccc cgg gag gtg gtg gtg ccc ttg act gtg gag ctc atg ggc acc 191  
 Gln Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr  
                     50                    55                    60  
 gtg gcc aaa cag ctg gtg ccc agc tgc gtg act gtg cag cgc tgt ggt 239  
 Val Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly  
                     65                    70                    75  
 ggc tgc tgc cct gac gat ggc ctg gag tgt gtg ccc act ggg cag cac 287  
 Gly Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His  
                     80                    85                    90                    95  
 caa gtc cgg atg cag atc ctc atg atc cgg tac ccg agc agt cag ctg 335  
 Gln Val Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu  
                     100                    105                    110  
 ggg gag atg tcc ctg gaa gaa cac agc cag tgt gaa tgc aga cct aaa 383  
 Gly Glu Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys Arg Pro Lys  
                     115                    120                    125  
 aaa aag gac agt gct gtg aag cca gat agg tgc cgg aag ctg cga agg 431  
 Lys Lys Asp Ser Ala Val Lys Pro Asp Arg Cys Arg Lys Leu Arg Arg  
                     130                    135                    140  
 tgacacatgg cttttcagac tcagcagggt gacttgcttc agaggctata tcccagtggg 491  
 ggaacaaagg ggagcctggt aaaaaacagc caagccccca agacctcagc ccaggcagaa 551  
 gctgctctag gacctggggc tctcagaggg ctcttctgcc atcccttgtc tccctgaggc 611  
 catcatcaaa caggacagag ttggaagagg agactgggag gcagcaagag gggtcacata 671  
 ccagctcagg ggagaatgga gtactgtctc agtttctaac cactctgtgc aagtaagcat 731  
 cttacaactg gctcttcttc cctcactaa gaagacccaa acctctgcat aatgggattt 791

gggcttttggg acaagaactg tgaccccccaa ccttgataaa agagatggaa ggaaaaaaaa 851

aaaaaaaa

858

<210> 8

<211> 143

<212> PRT

<213> Nuc. Seq. of SOM175 Absent Exons 6&7

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Met Ser Pro Leu Leu Arg Arg Leu Leu Leu Ala Ala Leu Leu Gln Leu  
1 5 10 15

Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His Gln  
20 25 30

Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys Gln  
35 40 45

Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr Val  
50 55 60

Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly Gly  
65 70 75 80

Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His Gln  
85 90 95

Val Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu Gly  
100 105 110

Glu Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys Arg Pro Lys Lys  
115 120 125

Lys Asp Ser Ala Val Lys Pro Asp Arg Cys Arg Lys Leu Arg Arg  
130 135 140

<210> 9

<211> 910

<212> DNA

<213> Nuc. Seq. of SOM175 Absent Exon 4

<220>

<221> CDS

<222> (3)...(305)

<400> 9

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Met Ser Pro Leu Leu Arg Arg Leu Leu Leu Ala Ala Leu Leu Gln  
1 5 10 15

ctg gcc ccc gcc cag gcc cct gtc tcc cag cct gat gcc cct ggc cac 95  
 Leu Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His  
                     20                    25                    30  
 cag agg aaa gtg gtg tca tgg ata gat gtg tat act cgc gct acc tgc 143  
 Gln Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys  
                     35                    40                    45  
 cag ccc cgg gag gtg gtg gtg ccc ttg act gtg gag ctc atg ggc acc 191  
 Gln Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr  
                     50                    55                    60  
 gtg gcc aaa cag ctg gtg ccc agc tgc gtg act gtg cag cgc tgt ggt 239  
 Val Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly  
                     65                    70                    75  
 ggc tgc tgc cct gac gat ggc ctg gag tgt gtg ccc act ggg cag cac 287  
 Gly Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His  
                     80                    85                    90                    95  
 caa gtc cgg atg cag acc taaaaaaaaag gacagtgctg tgaagccaga 335  
 Gln Val Arg Met Gln Thr  
                     100  
 cagggctgcc actccccacc accgtcccca gccccgttct gttccgggct gggactctgc 395  
 ccccgaggca cctccccag ctgacatcac ccatcccact ccagccccag gcccctctgc 455  
 ccacgctgca cccagcacca ccagcgccct gacccccgga cctgccgctg ccgctgccga 515  
 cgccgcagct tcctccgttg ccaagggcgg ggcttagagc tcaaccaga cacctgcagg 575  
 tgccggaagc tgcaaggtg acacatggct tttcagactc agcaggggtga cttgcctcag 635  
 aggctatatc ccagtgggga acaaagagga gcctggtaaa aaacagccaa gcccccaaga 695  
 cctcagccca ggcagaagct gctctaggac ctgggcctct cagagggctc ttctgccatc 755  
 ccttgtctcc ctgaggccat catcaaacag gacagagttg gaagaggaga ctgggaggca 815  
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tctgtgcaag taagcatctt acaactggct cttcc

910

<210> 10

<211> 101

<212> PRT

<213> Nuc. Seq. of SOM175 Absent Exon 4

<400> 10

Met Ser Pro Leu Leu Arg Arg Leu Leu Leu Ala Ala Leu Leu Gln Leu  
1 5 10 15

Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His Gln  
20 25 30

Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys Gln  
35 40 45

Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr Val  
50 55 60

Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly Gly  
65 70 75 80

Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His Gln  
85 90 95

Val Arg Met Gln Thr  
100

<210> 11

<211> 42

<212> DNA

<213> Oligonucleotide

<400> 11

accaccacct ccctgggctg gcatgtggca cgtgcataaa cg

42

<210> 12

<211> 42

<212> DNA

<213> Oligonucleotide

<400> 12

agttgtttga ccacattgcc catgagttcc atgctcagag gc

42

<210> 13

<211> 38

<212> DNA

<213> Oligonucleotide

<400> 13

gatacctgggg ctggagtggg atggatgatg tcagctgg

38

<210> 14

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<212> DNA

<213> Oligonucleotide

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<211> 236

<212> DNA

<213> Human SOM175

<400> 15

atgagggggcc aggtacgtga ggtctccac agggccctgg aaagaatact tacatctgct 60

cccatgggtgt atgcaggtcc gagatgctga atacagatcc tcatgcaggt gtcaggcaac 120

ttttcaagac ctaaagacag gtgagtcttt ctctccgta ggctgcctcc agccccaggc 180

ccccactcc agccccagac ccagacacct gtagccctgc tcaggtgccg aggtga 236

<210> 16

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<221> CDS

<222> (166)..(789)

<400> 16

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ggggggccgcg gaggagccgc cccctgcgcc ccgccccggg tccccgggtc cgcgccatgg 120

ggcggctctg gctgaccccc cccacaccg ccgggctagg gcccg atg agc ccc ctg 177

Met Ser Pro Leu

1

ctg cgt cgc ctg ctg ctt gtt gca ctg ctg cag ctg gct cgc acc cag 225

Leu	Arg	Arg	Leu	Leu	Leu	Val	Ala	Leu	Leu	Gln	Leu	Ala	Arg	Thr	Gln	
5					10					15					20	
gcc	cct	gtg	tcc	cag	ttt	gat	ggc	ccc	agt	cac	cag	aag	aaa	gtg	gtg	273
Ala	Pro	Val	Ser	Gln	Phe	Asp	Gly	Pro	Ser	His	Gln	Lys	Lys	Val	Val	
				25					30					35		
cca	tgg	ata	gac	gtt	tat	gca	cgt	gcc	aca	tgc	cag	ccc	agg	gag	gtg	321
Pro	Trp	Ile	Asp	Val	Tyr	Ala	Arg	Ala	Thr	Cys	Gln	Pro	Arg	Glu	Val	
			40					45					50			
gtg	gtg	cct	ctg	agc	atg	gaa	ctc	atg	ggc	aat	gtg	gtc	aaa	caa	cta	369
Val	Val	Pro	Leu	Ser	Met	Glu	Leu	Met	Gly	Asn	Val	Val	Lys	Gln	Leu	
		55					60					65				
gtg	ccc	agc	tgt	gtg	act	gtg	cag	cgc	tgt	ggc	ggc	tgc	tgc	cct	gac	417
Val	Pro	Ser	Cys	Val	Thr	Val	Gln	Arg	Cys	Gly	Gly	Cys	Cys	Pro	Asp	
	70					75					80					
gat	ggc	ctg	gaa	tgt	gtg	ccc	act	ggg	caa	cac	caa	gtc	cga	atg	cag	465
Asp	Gly	Leu	Glu	Cys	Val	Pro	Thr	Gly	Gln	His	Gln	Val	Arg	Met	Gln	
85					90					95					100	
atc	ctc	atg	atc	cag	tac	ccg	agc	agt	cag	ctg	ggg	gag	atg	tcc	ctg	513
Ile	Leu	Met	Ile	Gln	Tyr	Pro	Ser	Ser	Gln	Leu	Gly	Glu	Met	Ser	Leu	
				105					110					115		
gga	gaa	cac	agc	caa	tgt	gaa	tgc	aga	cct	aaa	aaa	aag	gag	agt	gct	561
Gly	Glu	His	Ser	Gln	Cys	Glu	Cys	Arg	Pro	Lys	Lys	Lys	Glu	Ser	Ala	
			120					125					130			
gtg	agg	cca	gac	agg	gtt	gcc	ata	ccc	cac	cac	cgt	ccc	cag	ccc	cgc	609
Val	Arg	Pro	Asp	Arg	Val	Ala	Ile	Pro	His	His	Arg	Pro	Gln	Pro	Arg	
		135				140						145				
tct	gtt	ccg	ggc	tgg	gac	tct	acc	ccg	gga	gca	ccc	tcc	cca	gct	gac	657
Ser	Val	Pro	Gly	Trp	Asp	Ser	Thr	Pro	Gly	Ala	Pro	Ser	Pro	Ala	Asp	
	150					155					160					
atc	atc	cat	ccc	act	cca	gcc	cca	gga	tcc	tct	gcc	cgc	ctt	gca	ccc	705
Ile	Ile	His	Pro	Thr	Pro	Ala	Pro	Gly	Ser	Ser	Ala	Arg	Leu	Ala	Pro	
165					170					175					180	
agc	gcc	gcc	aac	gcc	ctg	acc	ccc	gga	cct	gcc	gtt	gcc	gct	gta	gac	753
Ser	Ala	Ala	Asn	Ala	Leu	Thr	Pro	Gly	Pro	Ala	Val	Ala	Ala	Val	Asp	

185 190 195  
 gcc gcc gct tcc tcc att gcc aag ggc ggg gct tag agctcaaccc 799  
 Ala Ala Ala Ser Ser Ile Ala Lys Gly Gly Ala  
 200 205  
 agacacctgt aggtgccgga agccgcgaaa gtgacaagct gctttccaga ctccacgggc 859  
 ccggctgctt ttatggccct gcttcacagg gagaagagtg gagcacaggc gtaacctcct 919  
 cagtctggga ggtcactgcc ccaggacctg gaccttttag agagctctct cgccatcttt 979  
 tatctcccag agctgccatc taacaattgt caaggaacct catgtctcac ctccaggggcc 1039  
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 <211> 207  
 <212> PRT  
 <213> mVRF

<400> 17  
 Met Ser Pro Leu Leu Arg Arg Leu Leu Leu Val Ala Leu Leu Gln Leu  
 1 5 10 15  
 Ala Arg Thr Gln Ala Pro Val Ser Gln Phe Asp Gly Pro Ser His Gln  
 20 25 30  
 Lys Lys Val Val Pro Trp Ile Asp Val Tyr Ala Arg Ala Thr Cys Gln  
 35 40 45  
 Pro Arg Glu Val Val Val Pro Leu Ser Met Glu Leu Met Gly Asn Val  
 50 55 60  
 Val Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly Gly  
 65 70 75 80  
 Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His Gln  
 85 90 95  
 Val Arg Met Gln Ile Leu Met Ile Gln Tyr Pro Ser Ser Gln Leu Gly  
 100 105 110  
 Glu Met Ser Leu Gly Glu His Ser Gln Cys Glu Cys Arg Pro Lys Lys  
 115 120 125  
 Lys Glu Ser Ala Val Arg Pro Asp Arg Val Ala Ile Pro His His Arg  
 130 135 140

Pro Gln Pro Arg Ser Val Pro Gly Trp Asp Ser Thr Pro Gly Ala Pro  
 145 150 155 160  
 Ser Pro Ala Asp Ile Ile His Pro Thr Pro Ala Pro Gly Ser Ser Ala  
 165 170 175  
 Arg Leu Ala Pro Ser Ala Ala Asn Ala Leu Thr Pro Gly Pro Ala Val  
 180 185 190  
 Ala Ala Val Asp Ala Ala Ala Ser Ser Ile Ala Lys Gly Gly Ala  
 195 200 205

<210> 18  
 <211> 188  
 <212> PRT  
 <213> mVRF167

<400> 18  
 Met Ser Pro Leu Leu Arg Arg Leu Leu Leu Val Ala Leu Leu Gln Leu  
 1 5 10 15  
 Ala Arg Thr Gln Ala Pro Val Ser Gln Phe Asp Gly Pro Ser His Gln  
 20 25 30  
 Lys Lys Val Val Pro Trp Ile Asp Val Tyr Ala Arg Ala Thr Cys Gln  
 35 40 45  
 Pro Arg Glu Val Val Val Pro Leu Ser Met Glu Leu Met Gly Asn Val  
 50 55 60  
 Val Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly Gly  
 65 70 75 80  
 Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His Gln  
 85 90 95  
 Val Arg Met Gln Ile Leu Met Ile Gln Tyr Pro Ser Ser Gln Leu Gly  
 100 105 110  
 Glu Met Ser Leu Gly Glu His Ser Gln Cys Glu Cys Arg Pro Lys Lys  
 115 120 125  
 Lys Glu Ser Ala Val Arg Pro Asp Ser Pro Arg Ile Leu Cys Pro Pro  
 130 135 140  
 Cys Thr Gln Arg Arg Gln Arg Pro Asp Pro Arg Thr Cys Arg Cys Arg  
 145 150 155 160  
 Cys Arg Arg Arg Arg Phe Leu His Cys Gln Gly Arg Gly Leu Glu Leu  
 165 170 175  
 Asn Pro Asp Thr Cys Arg Cys Arg Lys Pro Arg Lys  
 180 185

<210> 19  
 <211> 188



<212> PRT  
<213> hVRF167

<400> 19

Met Ser Pro Leu Leu Arg Arg Leu Leu Leu Ala Ala Leu Leu Gln Leu  
1 5 10 15  
Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His Gln  
20 25 30  
Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys Gln  
35 40 45  
Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr Val  
50 55 60  
Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly Gly  
65 70 75 80  
Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His Gln  
85 90 95  
Val Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu Gly  
100 105 110  
Glu Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys Arg Pro Lys Lys  
115 120 125  
Lys Asp Ser Ala Val Lys Pro Asp Ser Pro Arg Pro Leu Cys Pro Arg  
130 135 140  
Cys Thr Gln His His Gln Arg Pro Asp Pro Arg Thr Cys Arg Cys Arg  
145 150 155 160  
Cys Arg Arg Arg Ser Phe Leu Arg Cys Gln Gly Arg Gly Leu Glu Leu  
165 170 175  
Asn Pro Asp Thr Cys Arg Cys Arg Lys Leu Arg Arg  
180 185

<210> 20  
<211> 71  
<212> PRT  
<213> mVRF186

<400> 20

Arg Val Ala Ile Pro His His Arg Pro Gln Pro Arg Ser Val Pro Gly  
1 5 10 15  
Trp Asp Ser Thr Pro Gly Ala Pro Ser Pro Ala Asp Ile Ile His Pro  
20 25 30  
Thr Pro Ala Pro Gly Ser Ser Ala Arg Leu Ala Pro Ser Ala Ala Asn  
35 40 45

Ala Leu Thr Pro Gly Pro Ala Val Ala Ala Val Asp Ala Ala Ala Ser  
 50 55 60

Ser Ile Ala Lys Gly Gly Ala  
 65 70

<210> 21  
 <211> 71  
 <212> PRT  
 <213> hVRF186

<400> 21  
 Arg Ala Ala Thr Pro His His Arg Pro Gln Pro Arg Ser Val Pro Gly  
 1 5 10 15

Trp Asp Ser Ala Pro Gly Ala Pro Ser Pro Ala Asp Ile Thr His Pro  
 20 25 30

Thr Pro Ala Pro Gly Pro Ser Ala His Ala Ala Pro Ser Thr Thr Ser  
 35 40 45

Ala Leu Thr Pro Gly Pro Ala Ala Ala Ala Ala Asp Ala Ala Ala Ser  
 50 55 60

Ser Val Ala Lys Gly Gly Ala  
 65 70

<210> 22  
 <211> 214  
 <212> PRT  
 <213> mVEGF188

<400> 22  
 Met Asn Phe Leu Leu Ser Trp Val His Trp Thr Leu Ala Leu Leu Leu  
 1 5 10 15

Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro Thr Thr Glu Gly  
 20 25 30

Glu Gln Lys Ser His Glu Val Ile Lys Phe Met Asp Val Tyr Gln Arg  
 35 40 45

Ser Tyr Cys Arg Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu Tyr  
 50 55 60

Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu Met  
 65 70 75 80

Arg Cys Ala Gly Cys Cys Asn Asp Glu Ala Leu Glu Cys Val Pro Thr  
 85 90 95

Ser Glu Ser Asn Ile Thr Met Gln Ile Met Arg Ile Lys Pro His Gln  
 100 105 110

Ser	Gln	His	Ile	Gly	Glu	Met	Ser	Phe	Leu	Gln	His	Ser	Arg	Cys	Glu
		115					120					125			
Cys	Arg	Pro	Lys	Lys	Asp	Arg	Thr	Lys	Pro	Glu	Lys	Lys	Ser	Val	Arg
	130					135					140				
Gly	Lys	Gly	Lys	Gly	Gln	Lys	Arg	Lys	Arg	Lys	Lys	Ser	Arg	Phe	Lys
145					150					155					160
Ser	Trp	Ser	Val	His	Cys	Glu	Pro	Cys	Ser	Glu	Arg	Arg	Lys	His	Leu
				165					170					175	
Phe	Val	Gln	Asp	Pro	Gln	Thr	Cys	Lys	Cys	Ser	Cys	Lys	Asn	Thr	Asp
			180					185					190		
Ser	Arg	Cys	Lys	Ala	Arg	Gln	Leu	Glu	Leu	Asn	Glu	Arg	Thr	Cys	Arg
		195					200					205			
Cys	Asp	Lys	Pro	Arg	Arg										
	210														